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#14

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/011,307

DATE: 09/08/2003
TIME: 13:26:27

Input Set : N:\EBONY'S\US09011307.raw.txt
Output Set: N:\CRF4\09082003\I011307.raw

SEQUENCE LISTING

1 (1) GENERAL INFORMATION:

2 (i) APPLICANT: Zabeau, Marc
3 Vos, Pieter
4 Simons, Guus
5 (ii) TITLE OF INVENTION: RESISTANCE AGAINST WILT INDUCING FUNGI
6 (iii) NUMBER OF SEQUENCES: 12
7 (iv) CORRESPONDENCE ADDRESS:
8 (A) ADDRESSEE: SPENCER & FRANK
9 (B) STREET: 1100 New York Avenue, N.W., Suite 300 East
10 (C) CITY: Washington
11 (D) STATE: DC
12 (E) COUNTRY: USA
13 (F) ZIP: 20005
14 (v) COMPUTER READABLE FORM:
15 (A) MEDIUM TYPE: Floppy disk
16 (B) COMPUTER: IBM PC compatible
17 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
18 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
19 (vi) CURRENT APPLICATION DATA:

C--> 20 (A) APPLICATION NUMBER: US/09/011,307
C--> 21 (B) FILING DATE: 01-Jul-1988
22 (C) CLASSIFICATION:

23 (vii) PRIOR APPLICATION DATA:
24 (A) APPLICATION NUMBER: EP 95401849.5
25 (B) FILING DATE: 07-AUG-1995

26 (viii) ATTORNEY/AGENT INFORMATION:
27 (A) NAME: Gollin, Michael A.
28 (B) REGISTRATION NUMBER: 31,957
29 (C) REFERENCE/DOCKET NUMBER: GUPLA 0008

30 (ix) TELECOMMUNICATION INFORMATION:
31 (A) TELEPHONE: 202-414-4000
32 (B) TELEFAX: 202-414-4040

33 (2) INFORMATION FOR SEQ ID NO: 1:
34 (i) SEQUENCE CHARACTERISTICS:
35 (A) LENGTH: 19 base pairs
36 (B) TYPE: nucleic acid
37 (C) STRANDEDNESS: single
38 (D) TOPOLOGY: linear

39 (ii) MOLECULE TYPE: other nucleic acid
40 (A) DESCRIPTION: /desc = "primer"
41 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
42 GACTGCGTAC CAATTCNNN

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44 (2) INFORMATION FOR SEQ ID NO: 2: 19
 45 (i) SEQUENCE CHARACTERISTICS:
 46 (A) LENGTH: 19 base pairs
 47 (B) TYPE: nucleic acid
 48 (C) STRANDEDNESS: single
 49 (D) TOPOLOGY: linear
 50 (ii) MOLECULE TYPE: other nucleic acid
 51 (A) DESCRIPTION: /desc = "primer"
 52 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
 53 GATGAGTCCT GAGTAANNN
 55 (2) INFORMATION FOR SEQ ID NO: 3: 17
 56 (i) SEQUENCE CHARACTERISTICS:
 57 (A) LENGTH: 17 base pairs
 58 (B) TYPE: nucleic acid
 59 (C) STRANDEDNESS: single
 60 (D) TOPOLOGY: linear
 61 (ii) MOLECULE TYPE: other nucleic acid
 62 (A) DESCRIPTION: /desc = "oligonucleotide"
 63 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
 64 CTCGTAGACT GCGTAC
 66 (2) INFORMATION FOR SEQ ID NO: 4: 18
 67 (i) SEQUENCE CHARACTERISTICS:
 68 (A) LENGTH: 18 base pairs
 69 (B) TYPE: nucleic acid
 70 (C) STRANDEDNESS: single
 71 (D) TOPOLOGY: linear
 72 (ii) MOLECULE TYPE: other nucleic acid
 73 (A) DESCRIPTION: /desc = "oligonucleotide"
 74 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
 75 AATTGGTACG CAGTCTAC
 77 (2) INFORMATION FOR SEQ ID NO: 5: 16
 78 (i) SEQUENCE CHARACTERISTICS:
 79 (A) LENGTH: 16 base pairs
 80 (B) TYPE: nucleic acid
 81 (C) STRANDEDNESS: single
 82 (D) TOPOLOGY: linear
 83 (ii) MOLECULE TYPE: other nucleic acid
 84 (A) DESCRIPTION: /desc = "oligonucleotide"
 85 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
 86 GACGATGAGT CCTGAG
 88 (2) INFORMATION FOR SEQ ID NO: 6: 16
 89 (i) SEQUENCE CHARACTERISTICS:
 90 (A) LENGTH: 14 base pairs
 91 (B) TYPE: nucleic acid
 92 (C) STRANDEDNESS: single
 93 (D) TOPOLOGY: linear
 94 (ii) MOLECULE TYPE: other nucleic acid
 95 (A) DESCRIPTION: /desc = "oligonucleotide"
 96 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

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97 TACTCAGGAC TCAT
99 (2) INFORMATION FOR SEQ ID NO: 7:
100 (i) SEQUENCE CHARACTERISTICS:
101 (A) LENGTH: 16 base pairs
102 (B) TYPE: nucleic acid
103 (C) STRANDEDNESS: single
104 (D) TOPOLOGY: linear
105 (ii) MOLECULE TYPE: other nucleic acid
106 (A) DESCRIPTION: /desc = "primer"
107 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
108 GACTGCGTAC CAATTC
109
110 (2) INFORMATION FOR SEQ ID NO: 8:
111 (i) SEQUENCE CHARACTERISTICS:
112 (A) LENGTH: 16 base pairs
113 (B) TYPE: nucleic acid
114 (C) STRANDEDNESS: single
115 (D) TOPOLOGY: linear
116 (ii) MOLECULE TYPE: other nucleic acid
117 (A) DESCRIPTION: /desc = "primer"
118 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
119 GATGAGTCCT GAGTAA
120
121 (2) INFORMATION FOR SEQ ID NO: 9:
122 (i) SEQUENCE CHARACTERISTICS:
123 (A) LENGTH: 19 base pairs
124 (B) TYPE: nucleic acid
125 (C) STRANDEDNESS: single
126 (D) TOPOLOGY: linear
127 (ii) MOLECULE TYPE: other nucleic acid
128 (A) DESCRIPTION: /desc = "primer"
129 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
130 GACTGCGTAC CAATTCA
131
132 (2) INFORMATION FOR SEQ ID NO: 10:
133 (i) SEQUENCE CHARACTERISTICS:
134 (A) LENGTH: 19 base pairs
135 (B) TYPE: nucleic acid
136 (C) STRANDEDNESS: single
137 (D) TOPOLOGY: linear
138 (ii) MOLECULE TYPE: other nucleic acid
139 (A) DESCRIPTION: /desc = "primer"
140 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:
141 GATGAGTCCT GAGTAATCT
142
143 (2) INFORMATION FOR SEQ ID NO: 11:
144 (i) SEQUENCE CHARACTERISTICS:
145 (A) LENGTH: 6658 base pairs
146 (B) TYPE: nucleic acid
147 (C) STRANDEDNESS: single
148 (D) TOPOLOGY: linear
149 (ii) MOLECULE TYPE: cDNA
150 (ix) FEATURE:

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151 (A) NAME/KEY: CDS
152 (B) LOCATION: 1798..5595
153 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:
154 AAAAAAGCAG CTTTAAAAAA AGTACTTKG AAAGGKGCTG AAACTTATT TTTGAAATAA 60
155 GCAGTTATGT GTTTGGAAWA AAAGTGCTGA AGTTGCTATG TCAAACATGA AAAGGGRAAA 120
156 AATGGAAGAA AGAGWTGTTA GGGTTATGTC GTAATTGGA GATTGTATAA AAATATTAAG 180
157 GGCAAAAAAA ATAAAAATGT GTCAACTTAA AACAGCTTAT AAGCTAAAAG TTAAAAGCTG 240
158 GGGTAGAGGT GTTTTTTTT TTTTAGCTT ATAAGTTGTT TTAAGTTGAC CACATTTTA 300
159 TTTTAKTTGC CCTTAATATT TTTATACAAT CTCAAAATTA CGACATAACC CTAACATCTT 360
160 TTTCTCCCAT TTTTCCTTT TCACGTTGA CATAGCAACT TCAGCACTT TATCCAAACA 420
161 CATAACTGCT TATTTAAAAA ATAAGTTCA GCACTTCAA AAGTACTTTT TTAAAGCTGC 480
162 TTTTATTAAG CCCATCCAAA CGGGCCCTAA AATTGCTAAT GTTGTCTTT TCTATTCTCA 540
163 AACTCCGTAA TATTTAAGAA AATTGCTAA TGATAGGTCA CTTTTAACAC TAAATAATTA 600
164 TAAATTGGGT AGAAATTAT TTATCATTAA AAGCTTTTT AATTGGAGT CTTCTCCCTA 660
165 ATTAAGACCC TTCCCCTCTT GCTTCATTA TTTAAGTCAA TAGTCTTTGT CTTATTGTTG 720
166 GGTGAAAGTC TGTCTCTTG TTAGGTACTA AGTCCTACAA TAATATCAAT AATTGCTAT 780
167 GGAGAAAAAA ATATTATAGG AGAAAATAA TTAATTAA TTCATGAATA TGTCTTAATA 840
168 TGCAACTCAT TTTGCTTATA TATATCAAAT TAAACTCTGT TCCTTTAACT TTTCCATG 900
169 AAGATACATT TTAATTATT TGATGAGGTT AGTTTGAAA TTATATATT AATAATGAAA 960
170 TGATATAACT TAAAAGAAGT TGTTGATAT CTTATCAGAA TCATGCAGGT ACTCATAATA 1020
171 TAAGAAATAA TTATGATGAA ATTATATAT GTTTTATGCA GAGATTATTACCGCATTGTT 1080
172 TACTGGGTT ATGTATTACT TATTCATCT TTTATCAGAA TGAAAATTA TCATTCAATA 1140
173 AGAAATCCAA TTCTGTTAA TTCAAAATAC AAACAATAAC ATTTCAAGA CCGATTTTT 1200
174 GCCCAAGAAT ATACAGTAA CATAATTATG ATATGGTAGG TCTCTTTAGT AATTGACCAA 1260
175 CAAGGATTGT GGTGGAGTGG GAAATACTCT TTAATACTTC ACCAAGAGGT CTCCAATTG 1320
176 AGCCCTGAA TACGAAATCG TCTTGTAG TATATACCCT AACCTAATAC AAAAATTAGT 1380
177 ATATTAGCCT TNACAGCTAA AATCTTGTG ACCTGTAAGT CACCGCAGGA CAAATTAC 1440
178 GTAACACCAA CTTATTCAATG ATATAATTGT CCCTTTAGC ACAGTAATAA TGAGGTGGGT 1500
179 AGAAATTAT TACTTGAGGG CCCTTTCTAC ACCCACCTT ATCTCTTGCA TTCAATTATT 1560
180 GAATTGAAGA AGTAATGAAA AAACAGACTC CATTGGATAA AGGACAGTTT GCAAACACAG 1620
181 CTGTAACAAT TTAGAGCACT AGCAAAATAG AGAGAGTTT GAGAGAAATT TTTGTTGCA 1680
182 AATTACTCTT AACCTTCAGC AGGTAAAATA AAGTTCTTAA CTGAGACTAT TTGAAGATAT 1740
183 ATTTGTTAA AGAACATATT TGTGTGTTTC CTTGTTTGC TTTGCAGAT TTGAGAA 1797
184 ATG GAG ATT GGC TTA GCA GTT GGT GCA TTT CTC TCC TCA GCT TTG 1845
185 Met Glu Ile Gly Leu Ala Val Gly Gly Ala Phe Leu Ser Ser Ala Leu
186 1 5 10 15
187 AAT GTT CTG TTT GAT AGG CTT GCT CCT AAC GGT GAT CTG CTC AAC ATG 1893
188 Asn Val Leu Phe Asp Arg Leu Ala Pro Asn Gly Asp Leu Leu Asn Met
189 20 25 30
190 TTT CGG AAG CAT AAG GAT CAT GTT AAG CTC TTA AAG AAG CTG AAA ATG 1941
191 Phe Arg Lys His Lys Asp His Val Lys Leu Leu Lys Leu Lys Met
192 35 40 45
193 ACT TTG CGT GGT ATT CAG ATT GTG CTA AGT GAT GCA GAG AAT AAG CAA 1989
194 Thr Leu Arg Gly Ile Gln Ile Val Leu Ser Asp Ala Glu Asn Lys Gln
195 50 55 60
196 GCA TCA AAT CCA TCT GTG AGA GAC TGG CTT AAT GAG CTT CGA GAT GCT 2037
197 Ala Ser Asn Pro Ser Val Arg Asp Trp Leu Asn Glu Leu Arg Asp Ala
198 65 70 75 80
199 GTC GAC TCT GCT GAA AAT TTA ATA GAA GAA GTC AAT TAT GAA GCT TTG 2085

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200	Val Asp Ser Ala Glu Asn Leu Ile Glu Glu Val Asn Tyr Glu Ala Leu	
201	85 90 95	
202	AGG CTT AAG GTG GAA GGT CAG CAT CAG AAT TTT TCA GAA ACA AGC AAC	2133
203	Arg Leu Lys Val Glu Gly Gln His Gln Asn Phe Ser Glu Thr Ser Asn	
204	100 105 110	
205	CAG CAA GTA AGT GAT GAT TTT TTC CTT AAC ATA AAG GAC AAG CTG GAA	2181
206	Gln Gln Val Ser Asp Asp Phe Phe Leu Asn Ile Lys Asp Lys Leu Glu	
207	115 120 125	
208	GAC ACT ATT GAA ACA TTA AAG GAT TTG CAA GAG CAA ATT GGT CTC CTT	2229
209	Asp Thr Ile Glu Thr Leu Lys Asp Leu Gln Glu Gln Ile Gly Leu Leu	
210	130 135 140	
211	GGC TTA AAG GAG TAT TTT GAT TCC ACG AAA CTA GAA ACT AGA AGA CCT	2277
212	Gly Leu Lys Glu Tyr Phe Asp Ser Thr Lys Leu Glu Thr Arg Arg Pro	
213	145 150 155 160	
214	TCA ACT TCT GTG GAT GAT GAA TCT GAT ATC TTT GGT AGG CAG AGC GAA	2325
215	Ser Thr Ser Val Asp Asp Glu Ser Asp Ile Phe Gly Arg Gln Ser Glu	
216	165 170 175	
217	ATA GAG GAT TTG ATT GAC CGT CTA TTG TCT GAA GGT GCA AGT GGG AAA	2373
218	Ile Glu Asp Leu Ile Asp Arg Leu Leu Ser Glu Gly Ala Ser Gly Lys	
219	180 185 190	
220	AAG CTG ACA GTA GTT CCT ATC GTT GGA ATG GGC GGC CAG GGC AAG ACA	2421
221	Lys Leu Thr Val Val Pro Ile Val Gly Met Gly Gly Gln Gly Lys Thr	
222	195 200 205	
223	ACA CTT GCT AAA GCC GTA TAC AAT GAT GAG AGG GTG AAG AAT CAT TTT	2469
224	Thr Leu Ala Lys Ala Val Tyr Asn Asp Glu Arg Val Lys Asn His Phe	
225	210 215 220	
226	GAT TTG AAA GCG TGG TAT TGC GTT TCT GAA GGA TTT GAT GCT TTG AGA	2517
227	Asp Leu Lys Ala Trp Tyr Cys Val Ser Glu Gly Phe Asp Ala Leu Arg	
228	225 230 235 240	
229	ATA ACA AAA GAA TTA CTC CAA GAA ATT GGC AAA TTT GAC TCG AAG GAT	2565
230	Ile Thr Lys Glu Leu Leu Gln Glu Ile Gly Lys Phe Asp Ser Lys Asp	
231	245 250 255	
232	GTC CAC AAC AAT CTT AAC CAG CTT CAA GTC AAA TTG AAG GAA AGT TTG	2613
233	Val His Asn Asn Leu Asn Gln Leu Gln Val Lys Leu Lys Glu Ser Leu	
234	260 265 270	
235	AAG GGA AAG AAG TTC CTT ATT GTT TTG GAT GAT GTG TGG AAT GAA AAT	2661
236	Lys Gly Lys Lys Phe Leu Ile Val Leu Asp Asp Val Trp Asn Glu Asn	
237	275 280 285	
238	TAC AAC GAG TGG AAT GAC TTG AGA AAT ATT TTT GCA CAA GGA GAT ATA	2709
239	Tyr Asn Glu Trp Asn Asp Leu Arg Asn Ile Phe Ala Gln Gly Asp Ile	
240	290 295 300	
241	GGA AGT AAG ATC ATT GTG ACG ACA CGC AAA GAC AGT GTT GCC TTG ATG	2757
242	Gly Ser Lys Ile Ile Val Thr Thr Arg Lys Asp Ser Val Ala Leu Met	
243	305 310 315 320	
244	ATG GGA AAT GAG CAA ATT CGC ATG GGC AAT TTG TCT ACC GAA GCC TCT	2805
245	Met Gly Asn Glu Gln Ile Arg Met Gly Asn Leu Ser Thr Glu Ala Ser	
246	325 330 335	
247	TGG TCT TTA TTT CAA AGA CAT GCA TTT GAA AAC ATG GAT CCT ATG GGA	2853
248	Trp Ser Leu Phe Gln Arg His Ala Phe Glu Asn Met Asp Pro Met Gly	

VERIFICATION SUMMARY

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Input Set : N:\EBONY'S\US09011307.raw.txt

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L:20 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:21 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]

STATISTICS SUMMARY

PATENT APPLICATION: US/09/011,307

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Input Set : N:\EBONY'S\US09011307.raw.txt
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Application Serial Number: US/09/011,307

Alpha or Numeric or Xml: Alpha

Application Class:

Application File Date: 07-01-1988

Art Unit: PCT

Software Application: PatentIN1.0

Total Number of Sequences: 12

Total Nucleotides: 6831

Total Amino Acids: 1266

Number of Errors: 0

Number of Warnings: 0

Number of Corrections: 2

MESSAGE SUMMARY

220 C: 2 (Keyword misspelled or invalid format)